

GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model  
Run on: July 3, 2005, 02:01:47 ; Search time 1635.59 Seconds  
(without alignments)  
3025.428 Million cell updates/sec

Title: US-10-814-858A-2  
Perfect score: 130  
Sequence: 1 tcaatatataggaagttc.....ttacatctagataaacaatg 130

Scoring table: IDENTITY NUC  
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:\*

- 1: gb\_est1:\*
- 2: gb\_est2:\*
- 3: gb\_hic:\*
- 4: gb\_est3:\*
- 5: gb\_est4:\*
- 6: gb\_est5:\*
- 7: gb\_est6:\*
- 8: gb\_gss1:\*
- 9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	48	36.9	654	9	CG206846
C 2	42.6	32.8	884	8	AZ679757
C 3	42.6	32.8	888	8	AZ550547
C 4	42.6	32.8	935	8	AZ684425
C 5	39.8	30.6	424	5	BP617758
C 6	39.8	30.6	1093	3	CR725951
C 7	39	30.0	490	8	AZ045132
C 8	38.8	29.8	821	8	BH249781
C 9	38.8	29.8	963	9	CNS03E20
C 10	38.2	29.4	523	1	AA846861
C 11	37.8	29.1	530	8	AZ522110
C 12	37.8	29.1	979	9	CNS04LX9
C 13	37.4	28.8	572	4	BJ485243
C 14	37.4	28.8	628	4	BJ389532
C 15	37.4	28.8	752	1	AV711184
C 16	37.2	28.6	917	9	CG953396
C 17	37	28.5	1067	9	CNS038JM
C 18	36.6	28.2	502	4	BI440260
C 19	36.6	28.2	893	8	AZ534920
C 20	36.6	28.2	898	8	AZ692862
C 21	36.6	28.2	1198	3	CR697279
C 22	36.6	28.2	1273	8	CL649111
C 23	36.4	28.0	513	8	AZ239942
C 24	36.4	28.0	2689	9	AG390466

25	36.2	27.8	495	9	CR358331	CR358331 Arabidops
C 26	36.2	27.8	670	9	CE140833	CE140833 tigr-gss
C 27	36.2	27.8	964	8	BZ695586	BZ695586 SP_BA006
C 28	36.2	27.8	1269	9	CG749985	CG749985 P044-2-F0
C 29	36.2	27.8	1616	9	CL647121	CL647121 CH213-131
C 30	36	27.7	183	6	CB101154	CB101154 K167C11.Y
C 31	36	27.7	261	6	CA802634	CA802634 sau39G05.
C 32	36	27.7	284	2	AW423991	AW423991 sh59b04.Y
C 33	36	27.7	522	8	AQ248025	AQ248025 HS_2015.A
C 34	36	27.7	681	1	AV317591	AV317591 AV317591
C 35	36	27.7	700	4	BG856147	BG856147 1024044G0
C 36	36	27.7	707	8	BH927322	BH927322 oeh93e02.
C 37	36	27.7	751	8	BH736173	BH736173 BOH083TF
C 38	36	27.7	892	8	AZ686660	AZ686660 ENTW81TF
C 39	36	27.7	905	9	CG438011	CG438011 OGTBK39TV
C 40	36	27.7	1032	9	CNS020IP	AL206745 Tetradon
C 41	36	27.7	1525	9	AG486059	AG486059 Mus muscu
C 42	35.8	27.5	397	8	AQ102186	AQ102186 HS_3035.A
C 43	35.8	27.5	420	5	BQ584505	BQ584505 E011861-0
C 44	35.8	27.5	538	7	CF755575	CF755575 lae43b11.
C 45	35.8	27.5	562	5	BP121578	BP121578 BP121578

ALIGNMENTS

RESULT 1  
LOCUS CG206846/c  
DEFINITION TOS0467 TAMU Rice Japonica Nipponbare BAC Library (Hind III) Oryza sativa (japonica cultivar-group) genomic clone TOSJNBh019110h, genomic survey sequence.  
ACCESSION CG206846  
VERSION CG206846.1 GI:34097907  
KEYWORDS GSS.  
SOURCE Oryza sativa (japonica cultivar-group)  
ORGANISM Oryza sativa (japonica cultivar-group)  
REFERENCE 1 (bases 1 to 654)  
AUTHORS Li, Y., Wu, C., Santos, T., Uhm, T., Liu, D. and Zhang, H.-B.  
TITLE BAC end sequences to close the gaps of a rice physical map at TAMU Unpublished (2003)  
JOURNAL  
COMMENT Contact: Wu C  
Department of Soil and Crop Sciences and Institute for Plant Genomics and Biotechnology  
Texas A & M University  
TAMU 2474, College Station, TX 77843-2474, USA  
Tel: 979 862 4800  
Fax: 979 862 4790  
Email: c-wu@neo.tamu.edu  
Seq primer: MJ3 universal Forward GTAAACGACGGCCAGT  
Class: BAC ends  
High quality sequence stop: 654.  
Location/Qualifiers  
1. .654  
/organism="Oryza sativa (japonica cultivar-group)"  
/mol\_type="genomic DNA"  
/cultivar="Nipponbare"  
/db\_xref="taxon:39947"  
/clone="TOSJNBh019110h"  
/tissue\_type="leaf"  
/lab\_host="E. coli DH10B"  
/clone\_lib="TAMU Rice Japonica Nipponbare BAC Library (Hind III)"  
/note="Vector: V41"

ORIGIN  
Query Match 36.9%; Score 48; DB 9; Length 654;  
Best Local Similarity 90.0%; Pred. No. 0.34;  
Matches 63; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

Qy	45	TGTCATTTCTCAACATTACCACAACAAACAACAACAACATTTATACAATTACTAT	104
Dδ	156	TCATTTTTTACAAACAATTACCAACAACAACAACAACAACAT--TACAATTACTAT	99
Qy	105	TTACAATTAC	114
Dδ	98	TTACAATTAC	89

RESULT 2  
AZ679757/c  
LOCUS  
DEFINITION ENT1U137F Entamoeba histolytica 884 bp DNA linear GSS 14-DEC-2000  
genomic, Genomic survey sequence.  
VERSION AZ679757  
KEYWORDS AZ679757.1 GI:11816903  
SOURCE GSS.  
ORGANISM Entamoeba histolytica  
Entamoeba histolytica  
Eukaryota; Entamoebidae; Entamoeba.  
REFERENCE 1 (bases 1 to 884)  
AUTHORS Loftus,B., Van Aken,S. and Fraser,C.  
TITLE Determination of clone end sequences from Entamoeba histolytica  
HMI-1MSS sheared DNA library  
JOURNAL Unpublished (2000)  
COMMENT Contact: Bernard

Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0208  
Fax: 301 838 3543  
Email: [bjloftus@tigr.org](mailto:bjloftus@tigr.org)  
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared  
DNA library  
Seq primer: M13-Forward  
Class: shotgun  
High quality sequence start: 15  
High quality sequence stop: 806.  
Location/Qualifiers

1. .884  
/organism="Entamoeba histolytica"  
/mol\_type="genomic DNA"  
/strain="HM1:IMSS"  
/db\_xref="taxon:5759"  
/clone\_lib="Entamoeba histolytica Sheared DNA"  
/note="Vector: pGDS1; Site 1: Bat I; Constructed at The  
Institute for Genomic Research (TIGR), Rockville, MD.  
Genomic DNA isolated from broth cultures of E. histolytica  
using a method described by Clark and Diamond (Clark,  
C.G. and Diamond, L.S. (1993) Entamoeba histolytica: a  
method for isolate identification. Exp. Parasitol.  
77:450.). The DNA was mechanically sheared to give a  
tight size distribution (~2 kb). The v + i method used for  
the library construction is described in detail in Smith,  
H.O. and Venter, J.C. (Making small insert libraries for  
whole genome shotgun sequencing projects. In Genome  
Sequencing: A Practical Approach, eds M. Vaudin and B.  
Barrell, Oxford University Press, 1993).

	Query Match	Best Local Similarity	32.8%;	Score 42.6;	DB 8;	Length 884;	
	Matches	61.1%;	Pred. No. 5.9;	Mismatches 0;	Indels 44;	Gaps 0;	
	Conservative	69;					
Qy	18	TTTCATTTTCATTTGGAAATGGACAGTGTGTGTCATTTCTCAACAATTAACCAACAACAACA	77				
Db	551	TTTATTTTCATATATCTCTATCACTAATCTAAATTTAGCAATCTAATCAAAACAGTAAA	492				
Qy	78	CAACAAACAACATTATACAATTTACTATTTTACAAATTACATCTAGATATAACAATG	130				
Db	451	CAACAAAATAATATTTTAAAGGAATTAATACAAAGAAATTTGTAATTAATAATG	439				

RESULT 3	
AZ550547/C	
LOCUS	
DEFINITION	

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE AUTHORS TITLE	JOURNAL COMMENT
<p>1. <i>Journal of the American Medical Association</i>, 1964, 191: 1001-1002.</p> <p>2. <i>Journal of the American Medical Association</i>, 1964, 191: 1001-1002.</p>	<p>1. <i>Journal of the American Medical Association</i>, 1964, 191: 1001-1002.</p> <p>2. <i>Journal of the American Medical Association</i>, 1964, 191: 1001-1002.</p>

FEATURES  
source

## ORIGIN

Query Match  
Best Local  
Matches

1	py
310	pb
78	py
250	b

RESULT 4  
ZZ684425/c  
OCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE

AZ550547  
ENTPFZ70TF Entamoeba histolytica Sheared DNA  
genomic, genomic survey sequence.  
27550547  
linear GSS 14-NOV-2000  
Entamoeba histolytica

A2550547.1 GI:11175848  
GSS.  
Entamoeba histolytica  
Entamoeba histolytica  
Eukaryota; Entamoebidae; Entamoeba.  
1. (bases 1 to 888)

Deutscher, S., van Aken, S. and Fraser, C.  
Determination of clone end sequences from *Entamoeba histolytica*  
HMI-1MSS sheared DNA library  
Unpublished (2000)  
Contact: Brendan J Loftus  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0208  
Fax: 301 838 3543

Email: [bjloftus@tigr.org](mailto:bjloftus@tigr.org)  
 Clones are derived from the Entamoeba histolytica HM1:IMSS sheared  
 DNA library  
 Clq primer: M13-Forward  
 Clq template: shotgun  
 High quality sequence start: 16  
 High quality sequence stop: 863.  
 Location/Qualifiers  
     1..888

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/organism="Entamoeba histolytica"
/mol_type="genomic DNA"
/strain="HMI:IMSS"
/db_xref="taxon:5759"
/clone_lib="Entamoeba histolytica Sheared DNA"
/notes="Vector: pHOsi; Site: 1; Bat I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The +1 method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaubin and B.
Barell, Oxford University Press, 1999)."
```

	32.8%	Score 42.6;	DB 8;	Length 888;
Similarity	61.1%	Pred No. 5.9;		
Conservative	0;	Mismatches	44;	Indels 0; Gaps 0;
<p> TTCAATTCATTGGAATGGACACGTGTTGTCATTCTTCAACAATTTACCACACACACAA 77         TTTATTTTCATATATPCTCTATCAACTAATCTAATTTAGCAAACTATCAAAACACGTAAA         CAACAAACACACATTATACAATTTACTATTTTCAATTTACATCTAGATAAACATG 130         CAACAAATAATATTTTAAAGGAAATAAATACAAAGAAATTTGTTAATTTAAATATG 198        </p>				

6684425 935 bp DNA linear GSS 14-DEC-2000  
 WTH899R Entamoeba histolytica Sheared DNA Entamoeba histolytica  
 6684425 genomic survey sequence.  
 6684425.1 GI:11821571  
 IS.  
 Entamoeba histolytica



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Db      483 TATTTAAAGTGAATACATTGTTTGTAGTAGACAAGTACTGAACTTGCAAAAGTAACAC 424
QY      65 CAACAACACAAACAAACAAACATTATATACAACTTACTATTACAAATTACATCTAGATAA 124
Db      423 CAAATATATAGAAACCACTTAAATAAAGATGCCTCAAAATCTACAAATATTTCCAAATA 364
QY      125 ACA 127
Db      363 AAA 361

RESULT 7
LOCUS  A2045132
DEFINITION  Gm_UMB001_025_G19F UMN Soybean BAC Library (pECSBAC4 EcoRI) Glycine max genomic clone Glycine max genomic clone Gm_UMB001_025_G19, genomic survey sequence.
ACCESSION  A2045132
VERSION    A2045132.1 GI:7191282
KEYWORDS   GSS.
SOURCE     Glycine max (soybean)
ORGANISM   Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE  1 (bases 1 to 490)
AUTHORS   Larson,K., Mudge,J., Cooper,A., Grivna,S., Denny,R., Penuela,S., Danesh,D. and Young,N.D.
TITLE     BAC End sequences from a soybean genomic library (UMN)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Young Nevin D
            Department of Plant Pathology
            University of Minnesota
            495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul MN 55108, USA
            Tel: 612 625 2225
            Fax: 612 625 9728
            Email: nevin@cc.umn.edu
            Sequence on contig Gm_A963.ctg a near mapped duplicate of RFLP probe pA963 on linkage group F. For more information, see Soybase at: http://soybase.agron.iastate.edu. Please see as an authority for the mapping/naming: Cregan P.B., T. Jarvik, A.L. Bush, R.C. Shoemaker, K.G. Lark, A.L. Kahler, N. Kaya, T.T. Vantoi, D.G. Lohnes, J. Chung, and J.E. Specht. 1999a. An integrated genetic linkage map of the soybean genome. Crop Sci. 39:1464-1490
            Seq primer: M13F
            Class: BAC ends.
FEATURES   Location/Qualifiers
            source          1..490
                        /organism="Glycine max"
                        /mol_type="genomic DNA"
                        /cultivar="Faribault"
                        /db_xref="taxon:3847"
                        /clone="Gm_UMB001_025_G19"
                        /tissue_type="cotyledon leaves"
                        /dev_stage="cotyledon"
                        /clone_lib="UMN Soybean BAC Library (pECSBAC4 EcoRI)"
                        /note="Vector: pECSBAC4; The UMN BAC library (Danesh et al., Theor. Appl. Genet. 96:196, 1998), was constructed using the Eco RI site of pECSBAC4. The library consists of 72,960 clones with an average insert size of 120 kb, equal to 7 haploid genome equivalents. Screening of the library is done by hybridization of high-density colony filters and/or PCR amplification of DNA pools. Four high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening"

ORIGIN
Query Match      30.0%; Score 39; DB 8; Length 490;
Best Local Similarity 55.6%; Pred. No. 40;
Matches 69; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

LOCUS  A2045132
DEFINITION  Gm_UMB001_025_G19F UMN Soybean BAC Library (pECSBAC4 EcoRI) Glycine max genomic clone Glycine max genomic clone Gm_UMB001_025_G19, genomic survey sequence.
ACCESSION  A2045132
VERSION    A2045132.1 GI:7191282
KEYWORDS   GSS.
SOURCE     Glycine max (soybean)
ORGANISM   Glycine max
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
REFERENCE  1 (bases 1 to 490)
AUTHORS   Larson,K., Mudge,J., Cooper,A., Grivna,S., Denny,R., Penuela,S., Danesh,D. and Young,N.D.
TITLE     BAC End sequences from a soybean genomic library (UMN)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Young Nevin D
            Department of Plant Pathology
            University of Minnesota
            495 Borlaug Hall, 1991 Upper Buford Circle, St. Paul MN 55108, USA
            Tel: 612 625 2225
            Fax: 612 625 9728
            Email: nevin@cc.umn.edu
            Sequence on contig Gm_A963.ctg a near mapped duplicate of RFLP probe pA963 on linkage group F. For more information, see Soybase at: http://soybase.agron.iastate.edu. Please see as an authority for the mapping/naming: Cregan P.B., T. Jarvik, A.L. Bush, R.C. Shoemaker, K.G. Lark, A.L. Kahler, N. Kaya, T.T. Vantoi, D.G. Lohnes, J. Chung, and J.E. Specht. 1999a. An integrated genetic linkage map of the soybean genome. Crop Sci. 39:1464-1490
            Seq primer: M13F
            Class: BAC ends.
FEATURES   Location/Qualifiers
            source          1..490
                        /organism="Glycine max"
                        /mol_type="genomic DNA"
                        /cultivar="Faribault"
                        /db_xref="taxon:3847"
                        /clone="Gm_UMB001_025_G19"
                        /tissue_type="cotyledon leaves"
                        /dev_stage="cotyledon"
                        /clone_lib="UMN Soybean BAC Library (pECSBAC4 EcoRI)"
                        /note="Vector: pECSBAC4; The UMN BAC library (Danesh et al., Theor. Appl. Genet. 96:196, 1998), was constructed using the Eco RI site of pECSBAC4. The library consists of 72,960 clones with an average insert size of 120 kb, equal to 7 haploid genome equivalents. Screening of the library is done by hybridization of high-density colony filters and/or PCR amplification of DNA pools. Four high density filters, each containing 18,432 clones (doubly spotted), represent the whole library for colony screening"

ORIGIN
Query Match      30.0%; Score 39; DB 8; Length 490;
Best Local Similarity 55.6%; Pred. No. 40;
Matches 69; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

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QY      5 TATATATAGGAAGTTTCATTTTCATTTTGGAAATGGACACGTGTGTGTCATTTCTCAACAATTAC 64
Db      250 TATATATATGACATAATATTTTCTGGGTAGCGGANNNGTGTGACAACTTGGACACCTAT 309
QY      65 CAACAACACAAACAAACAAACATTATATACAACTTACTATTACAACTTACATCTAGATAA 124
Db      310 CTACCATATAGACAGAAAAAAGATTGAAATTTACAATCTAAAATNNAATAACAAA 369
QY      125 ACAA 128
Db      370 ATAA 373

RESULT 8
LOCUS  BH249781
DEFINITION  BH249781 821 bp DNA linear GSS 26-NOV-2001
            BOGAY07TF BOGA Brassica oleracea genomic clone BOGAY07, genomic survey sequence.
ACCESSION  BH249781
VERSION    BH249781.1 GI:17072773
KEYWORDS   GSS.
SOURCE     Brassica oleracea
ORGANISM   Brassica oleracea
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
REFERENCE  1 (bases 1 to 821)
AUTHORS   Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
TITLE     Whole genome shotgun sequencing of Brassica oleracea
JOURNAL   Unpublished (2001)
COMMENT   Other GSSs: BOGAY07TR
            Contact: Chris Town
            TIGR
            9712 Medical Center Drive, Rockville, MD 20850, USA.
            Tel: 301-838-3523
            Fax: 301-838-0208
            Email: cdtown@tigr.org
            DNA is from a doubled haploid provided by Tom Osborn.
            Seq primer: TF
            Class: sheared ends.
FEATURES   Location/Qualifiers
            source          1..821
                        /organism="Brassica oleracea"
                        /mol_type="genomic DNA"
                        /strain="TO1000DH3"
                        /db_xref="taxon:3712"
                        /clone="BOGAY07"
                        /clone_lib="BOGA"
                        /note="Vector: PHOS1; Site_1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers"

ORIGIN
Query Match      29.8%; Score 38.8; DB 8; Length 821;
Best Local Similarity 57.4%; Pred. No. 44;
Matches 70; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY      7 TATATAGGAAGTTTCATTTTCATTTTGGAAATGGACACGTGTGTGTCATTTCTCAACAATTACCA 66
Db      307 TAAATAGGTCGTACATTAGCTATGAAATTTACCTCTTTTATTATTACAGAAATTAATAA 366
QY      67 ACAACAACAACAACAACAACATTTATACAACTTACTATTACAACTTACATCTAGATAAAC 126
Db      367 ATATAATTTAAAAATACATAAATTTATTATTATTATTAATAAATTAATAATTAATAA 426
QY      127 AA 128
Db      427 AA 428

RESULT 9
LOCUS  CNS03E20
DEFINITION  CNS03E20 963 bp DNA linear GSS 01-SEP-2000
            CNS03E20/c

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/organism="Hordeum vulgare subsp. spontaneum"

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/note="Genoscope sequence in . contig. seq. file"
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/note="Genoscope sequence in . contig. seq. file"
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/mol_type="mRNA"
/strain="H602"
/sub_species="spontaneum"
/db_xref="taxon:77009"
/clone="bah54ml1"
/tissue_types="top three leaves"
/dev_stage="adult, heading stage"
/clone_lib="K. Sato unpublished cDNA library, strain H602
adult, heading stage top three leaves"

ORIGIN
Query Match      28.8%; Score 37.4; DB 4; Length 572;
Best Local Similarity 57.1%; Pred. No. 94;
Matches 68; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 8 ATATAGGAAGTTCATTTTCATTTGGAATGGACACGCTGTTGTCATTTCTCAACAATACCAA 67
    |||||
Db 563 ATGGAGGAGTATATACATATTAATGTCAGCTTGTGCTAGGTCTCACTAAGAA 504
    |||||

QY 68 CAACAACAACAACAACAATATACATTTACTATTACATTTACATTTACATTTACATTTACATTTAC 126
    |||||
Db 503 AAAAAACATCACTAAGAAAAAACAATCACTAAGAAAAAACAATCACTGTTGACACACC 445
    |||||

RESULT 14
BJ389532
LOCUS
DEFINITION BJ389532 Dictyostelium discoideum cDNA library, SF Dictyostelium
discoideum cDNA clone dds19i03 5', mRNA sequence.
ACCESSION BJ389532
VERSION BJ389532
KEYWORDS
SOURCE Dictyostelium discoideum
ORGANISM Dictyostelium discoideum
REFERENCE Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium.
AUTHORS Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-i,T.
TITLE Full length cDNA of Dictyostelium discoideum at the slug stage
JOURNAL Unpublished (2002)
COMMENT Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tehini@genes.nig.ac.jp.
Location/Qualifiers
1. .628
/organism="Dictyostelium discoideum"
/mol_type="mRNA"
/strain="AX4"
/db_xref="taxon:44689"
/clone="dds19i03"
/sex="mat A"
/dev_stage="slug stage"
/clone_lib="Dictyostelium discoideum cDNA library, SF"

ORIGIN
Query Match      28.8%; Score 37.4; DB 4; Length 628;
Best Local Similarity 55.9%; Pred. No. 93;
Matches 71; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

QY 3 ACTATATATAGGAAGTTCATTTTCATTTGGAATGGACACGCTGTTGTCATTTCTCAACAAT 62
    |||||
Db 70 AATATAGTAAAGAAATTTAAATTTATTTAAATAGAGTTATTGTAGTGGTTTCAAAAAT 129
    |||||

QY 63 ACCAACAACAACAACAACAATATACATTTACTATTACATTTACATTTACATTTACATTTACATTT 122
    |||||
Db 130 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 199
    |||||

QY 123 AAACAAT 129.
    |||||
Db 190 AGAGATT 196
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ACCESSION AV711184
VERSION AV711184
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 752)
AUTHORS Peng,Y., Song,H., Gu,Y., Yang,Y., Gao,G., Xiao,H., Xu,X., Li,N.,
Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z., Zeng,L., Xu,S.,
Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu,G., Hu,R.,
Chen,J., Chen,Z. and Han,Z.
Homo sapiens cDNA Cu clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
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QY 78 CAACAACAACAATATACAAATTACTATTACAAATTACATTTACATTTACATTTACATTTACAA 128
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